SEQUENCE LISTING

<110> MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.
     NATIONAL PUBLIC HEALTH INSTITUTE
     PELTONEN, Leena
     AALTONEN, Johanna
     BJORSES, Petra
     PERHEENTUPA, Jaakko
     PALOTIE, Aarno
     HORELLI-KUITUNEN, Nina
     YASPO, Marie-Laure
     LEHRACH, Hans

<120> NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN MUTATED
FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL DYSTROPHY (APECED)

<130> VOSS1130

<140> US 09/509,595
<141> 2000-07-05

<150> EP 97117154.1
<151> 1997-10-02

<150> EP 97117398.4
<151> 1997-10-08

<150> EP 97119810.6
<151> 1997-11-12

<160> 30

<170> PatentIn version 3.0

<210> 1
<211> 2245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (121)..(1758)

<400> 1
cgggcgcaca gccggcgcgg aggccccaca gccccgccgg gacccgaggc caagcgaggg   60

gctgccagtg tcccgggacc caccgcgtcc gccccagccc cgggtccccg cgcccaccc   120

atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg ctg cac cgc acg   168
Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1   5   10   15

gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg ctg cac gcg ctg   216
Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
            20   25   30

gct gac cac gac gtg gtc ccc gag gac aag ttt cag gag acg ctt cat   264
Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
        35   40   45

ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac gcc ctc ctg tcc   312
Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser

```
                50                     55                      60

tgg ctg ctg acc cag gac tcc aca gcc atc ctg gac ttc tgg agg gtg        360
Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65                  70                  75                  80

ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg ctg cag ccc atc        408
Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
                    85                  90                  95

ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag ccc cgg aag ggg        456
Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
                100                 105                 110

agg aag ccc ccg gcc gtc ccc aag gct ttg gta ccg cca ccc aga ctc        504
Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
                115                 120                 125

ccc acc aag agg aag gcc tca gaa gag gct cga gct gcc gcg cca gca        552
Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
            130                 135                 140

gcc ctg act cca agg ggc acc gcc agc cca ggc tct caa ctg aag gcc        600
Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145                 150                 155                 160

aag ccc ccc aag aag ccg gag agc agc gca gag cag cag cgc ctt cca        648
Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
                165                 170                 175

ctc ggg aac ggg att cag acc atg tca gct tca gtc cag aga gct gtg        696
Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
                180                 185                 190

gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg gcc gtg gag ggg        744
Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
                195                 200                 205

atc ctc atc cag cag gtg ttt gag tca ggc ggc tcc aag aag tgc atc        792
Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
            210                 215                 220

cag gtt ggt ggg gag ttc tac act ccc agc aag ttc gaa gac tcc ggc        840
Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
225                 230                 235                 240

agt ggg aag aac aag gcc cgc agc agc agt ggc ccg aag cct ctg gtt        888
Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
                245                 250                 255

cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga ggt gag gct agg        936
Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
                260                 265                 270

ctg ggc cag cag ggc agc gtt ccc gcc cct ctg gcc ctc ccc agt gac        984
Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
            275                 280                 285

ccc cag ctc cac cag aag aat gag gac gag tgt gcc gtg tgt cgg gac       1032
Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
            290                 295                 300
```

```
ggc ggg gag ctc atc tgc tgt gac ggc tgc cct cgg gcc ttc cac ctg          1080
Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
305                 310                 315                 320

gcc tgc ctg tcc cct ccg ctc cgg gag atc ccc agt ggg acc tgg agg          1128
Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
                325                 330                 335

tgc tcc agc tgc ctg cag gca aca gtc cag gag gtg cag ccc cgg gca          1176
Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
                340                 345                 350

gag gag ccc cgg ccc cag gag cca ccc gtg gag acc ccg ctc ccc ccg          1224
Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
                355                 360                 365

ggg ctt agg tcg gcg gga gag gag gta aga ggt cca cct ggg gaa ccc          1272
Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
        370                 375                 380

cta gcc ggc atg gac acg act ctt gtc tac aag cac ctg ccg gct ccg          1320
Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
385                 390                 395                 400

cct tct gca gcc ccg ctg cca ggg ctg gac tcc tcg gcc ctg cac ccc          1368
Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
                405                 410                 415

cta ctg tgt gtg ggt cct gag ggt cag cag aac ctg gct cct ggt gcg          1416
Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
                420                 425                 430

cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg cgg tgt act cac          1464
Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
                435                 440                 445

tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca gcc ggc acc tcc          1512
Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
        450                 455                 460

cgg ccc ggg acg ggc ctg cgc tgc aga tcc tgc tca gga gac gtg acc          1560
Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
465                 470                 475                 480

cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc gcc cgc ctg gcc          1608
Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
                485                 490                 495

cct ggg cct gcc aag gat gac act gcc agt cac gag ccc gct ctg cac          1656
Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
                500                 505                 510

agg gat gac ctg gag tcc ctt ctg agc gag cac acc ttc gat ggc atc          1704
Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
                515                 520                 525

ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg gcc ccc ttc ccc          1752
Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
        530                 535                 540
```

```
tcc tga ccccaga tgg ccgggaca tg cagctctga t gagagagtgc tgagaaggac          1808
Ser
545

acctccttcc tcag tcctgg aagcc ggccg gctggg atca agaaggg gac agcgccac ct      1868

cttgtcagtg ctcg gctgta aacag ctctg tgtttc tggg gacacca gcc atcatgtg cc      1928

tggaaattaa accc tgcccc acttc tctac tctgga agtc cccggga gcc tctccttg cc      1988

tggtgaccta ctaa aaatat aaaaa ttagc tgggtg tggt ggtgggt gcc tgtaatcc ca      2048

gctacatggg agcc tgaggc atgag aatca cttgaa ctcg ggaggtg gag gttgcagt ga      2108

gctgagattg cgcc actgca ctcca gtctg gtcggc aaga gtgagac tcc gtctcaaa aa      2168

caaaacaaaa aaac cacata acata aattt atcatc tcga ccacttt tca gttcagtg gc      2228

attcacatct catg taa                                                        2245
```

<210> 2
<211> 545
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1               5                   10                  15


Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
            20                  25                  30


Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
            35                  40                  45


Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
    50                  55                  60


Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65                  70                  75                  80


Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
                85                  90                  95


Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
                100                 105                 110


Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
            115                 120                 125


Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
```

```
            130                      135                      140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145              150              155                      160


Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
             165              170              175


Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
             180              185              190


Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
         195              200              205


Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
    210              215              220


Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
225              230              235              240


Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
             245              250              255


Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
             260              265              270


Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
             275              280              285


Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
    290              295              300


Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
305              310              315              320


Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
             325              330              335


Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
             340              345              350


Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
             355              360              365


Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
370              375              380
```

```
Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
385                 390             395             400


Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
                405             410                 415


Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
            420                 425                 430


Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
            435                 440                 445


Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
        450             455                 460


Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
465                 470                 475                 480


Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
                485                 490                 495


Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
            500                 505                 510


Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
            515                 520                 525


Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
        530                 535                 540


Ser
545


<210>  3
<211>  90
<212>  DNA
<213>  Murine

<400>  3
gtgtggactg tcacggaaac ccccacgtgt gatggaaagt ccaaaattct acaggagtct      60

ttctgttgat ctccagtcag aggctggggg                                      90


<210>  4
<211>  90
<212>  DNA
<213>  Homo sapiens
```

<400> 4
aaggggctgg tgtggaaagc cccacggcat ggtggaaagt ccgaaattct acaggggcct   60

ctttgttaaa cctccatgca agaggctggg   90

<210> 5
<211> 90
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(90)
<223> n is any nucleotide or a gap

<400> 5
nngnggnnng tnnngnaanc cccnnngnnt gntggaaagt ccnaaattct acaggngnct   60

ntntgttnan cnncnntnnn agnnnnnggg   90

<210> 6
<211> 1656
<212> DNA
<213> Murine

<220>
<221> CDS
<222> (1)..(1656)

<400> 6
atg gca ggt ggg gat gga atg cta cgc cgt ctg ctg agg ctg cac cgc   48
Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
1   5   10   15

acc gag atc gcg gtg gcc ata gac agt gcc ttt ccg ctg ctg cat gct   96
Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
                20   25   30

cta gcc gac cac gac gtg gtc cct gag gac aag ttc cag gag acg ctc   144
Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
            35   40   45

cgt ctg aag gag aag gaa ggc tgc ccc cag gcc ttc cac gcc ctg ctg   192
Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
        50   55   60

tcc tgg ctc ctg acc cgg gac agt ggg gcc atc ctg gat ttc tgg agg   240
Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
65   70   75   80

att ctc ttt aag gac tac aat ctg gag cgg tac agc cgc ctg cat agc   288
Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
                85   90   95

atc ctg gac ggc ttc cca aaa gat gtg gac cta aac cag tcc cgg aaa   336
Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
                100   105   110

```
ggg aga aag ccc ctt gct ggt ccc aag gcc gcg gta ctg cca ccc aga    384
Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
        115             120             125

ccc ccc acc aag aga aaa gca ctg gag gag cct cga gcc acc cca cca    432
Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
        130             135             140

gca act ctg gcc tca aag agc gtc tcc agc cca ggc tcc cac ctg aag    480
Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
145             150             155             160

act aag ccc cct aag aag cca gat ggc aac ttg gag tca cag cac ctt    528
Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
                165             170             175

cct ctt gga aac gga att cag acc atg gca gct tct gtc cag aga gct    576
Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
                180             185             190

gtg acc gtg gcc tct ggg gat gtt cca gga acc cga ggg gcc gtg gaa    624
Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
                195             200             205

ggg atc ctt atc cag cag gtg ttt gag tca gga aga tcc aag aag tgc    672
Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
        210             215             220

att cag gtt ggg gga gag ttt tat aca ccc aac aag ttc gaa gac ccc    720
Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
225             230             235             240

agt ggc aat ttg aag aac aag gcc cgg agt ggt agc agc cta aag cca    768
Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
                245             250             255

gtg gtc cga gcc aag gga gcc cag gtc act ata cct ggt aga gat gag    816
Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
                260             265             270

cag aaa gtg ggc cag cag tgt ggg gtt cct ccc ctt cca tcc ctc ccc    864
Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
                275             280             285

agt gag ccc cag gtt aac cag aag aac gag gat gag tgt gcc gtg tgc    912
Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
        290             295             300

cac gac gga ggt gag ctc atc tgt tgt gac ggc tgt ccc cgg gcc ttc    960
His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
305             310             315             320

cac ctg gct tgc ctg tcc cca cct ctg cag gag atc ccc agt ggc ctc   1008
His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
                325             330             335

tgg aga tgc tcc tgc tgc ctc cag ggc aga gtc caa cag aac ctg tcc   1056
Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
                340             345             350

cag cct gag gtg tcc agg ccc ccg gag cta cct gca gag acc ccg atc   1104
```

```
Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
        355                 360             365
```

```
ctc gtg gga ctg agg tca gct tca gag aaa acc agg ggc cca tcc agg    1152
Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
        370                 375             380
```

```
gag ctc aaa gcc agc tct gat gct gct gtc aca tat gtg aac ctg ctg    1200
Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
385                 390             395                 400
```

```
gcc ccg cac cct gca gct cct ctg ctg gag cct tca gca ctg tgc cct    1248
Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
                405             410             415
```

```
cta ctg agt gct ggg aat gag ggg cgg cca ggt cca gca cca agc gcg    1296
Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
            420                 425             430
```

```
cga tgc agt gtg tgt ggc gat ggc acc gag gtg ttg cgg tgt gca cac    1344
Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
            435                 440             445
```

```
tgt gcc gct gcc ttc cac tgg cgc tgc cac ttc ccg acg gcc gcc gcc    1392
Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
        450                 455             460
```

```
cgg ccg ggg acc aat ctc cgc tgc aaa tcc tgc tct gca gac tcg act    1440
Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
465                 470             475                 480
```

```
ccc acg cca ggc aca ccg ggc gaa gct gta ccc acc tct ggg ccc cgt    1488
Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
                485             490             495
```

```
cca gca cct ggg ctt gcc aag gta ggg gac gac tct gct agt cac gac    1536
Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
                500             505             510
```

```
cct gtt cta cat agg gac gac ctg gag tcc ctc ctc aat gag cac tca    1584
Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
            515                 520             525
```

```
ttt gac ggc atc ctg cag tgg gcc atc cag agc atg tca cgc ccg ctg    1632
Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
        530                 535             540
```

```
gcc gag aca cca ccc ttc tct tcc                                    1656
Ala Glu Thr Pro Pro Phe Ser Ser
545                 550
```

```
<210>  7
<211>  552
<212>  PRT
<213>  Murine

<400>  7

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
1               5               10              15
```

```
Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
            20              25              30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
            35              40              45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
    50              55              60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
65              70              75              80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
            85              90              95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
            100             105             110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
            115             120             125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
    130             135             140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
145             150             155             160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
            165             170             175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
            180             185             190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
            195             200             205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
    210             215             220

Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
225             230             235             240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
            245             250             255
```

Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
            260   265   270

Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
            275   280   285

Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
            290   295   300

His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
305   310   315   320

His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
            325   330   335

Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
            340   345   350

Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
            355   360   365

Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
            370   375   380

Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
385   390   395   400

Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
            405   410   415

Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
            420   425   430

Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
            435   440   445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
            450   455   460

Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
465   470   475   480

Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
            485   490   495

```
Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
            500                 505                 510


Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
            515                 520                 525


Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
            530                 535                 540


Ala Glu Thr Pro Pro Phe Ser Ser
545                 550


<210>   8
<211>   545
<212>   PRT
<213>   Homo sapiens

<400>   8

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1               5               10              15

Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
            20              25              30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
            35              40              45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
    50              55              60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65              70              75              80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
            85              90              95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
            100             105             110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
    115             120             125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
    130             135             140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145             150             155             160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
            165             170             175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
            180             185             190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
            195             200             205
```

```
Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
    210             215             220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
225             230             235                 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
            245             250             255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
            260             265             270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
            275             280             285

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
    290             295             300

Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
305             310             315             320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
            325             330             335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
            340             345             350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
            355             360             365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
    370             375             380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
385             390             395             400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
            405             410             415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
            420             425             430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
            435             440             445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
    450             455             460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
465             470             475             480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
            485             490             495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
            500             505             510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
    515             520             525
```

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
   530   535   540

Ser
545

<210> 9
<211> 552
<212> PRT
<213> Murine

<400> 9

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
1   5   10   15

Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
       20   25   30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
       35   40   45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
       50   55   60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
65   70   75   80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
         85   90   95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
       100   105   110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
       115   120   125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
       130   135   140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
145   150   155   160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
         165   170   175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
       180   185   190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
       195   200   205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
       210   215   220

Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
225   230   235   240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
       245   250   255

```
Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
            260             265             270

Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
            275             280             285

Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
    290             295             300

His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
305             310             315             320

His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
            325             330             335

Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
            340             345             350

Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
            355             360             365

Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
            370             375             380

Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
385             390             395             400

Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
            405             410             415

Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
            420             425             430

Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
            435             440             445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
    450             455             460

Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
465             470             475             480

Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
            485             490             495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
            500             505             510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
            515             520             525

Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
    530             535             540

Ala Glu Thr Pro Pro Phe Ser Ser
545             550
```

<210> 10
<211> 550
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus sequence of SEQ ID NO.:8 and SEQ ID NO.:9

<220>
<221> VARIANT
<222> (1)..(550)
<223> Xaa denotes any amino acid

<400> 10

```
Xaa Xaa Xaa Asp Xaa Xaa Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1               5                   10                  15

Glu Ile Ala Val Ala Xaa Asp Ser Ala Phe Pro Leu Leu His Ala Leu
            20                  25                  30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu Xaa
            35                  40                  45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
        50                  55                  60

Trp Leu Leu Thr Xaa Asp Ser Xaa Ala Ile Leu Asp Phe Trp Arg Xaa
65                  70                  75                  80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Xaa Arg Leu Xaa Xaa Ile
                85                  90                  95

Leu Asp Xaa Phe Pro Lys Asp Val Asp Leu Xaa Gln Xaa Arg Lys Gly
            100                 105                 110

Arg Lys Pro Xaa Ala Xaa Pro Lys Ala Xaa Val Xaa Pro Pro Arg Xaa
            115                 120                 125

Pro Thr Lys Arg Lys Ala Xaa Glu Glu Xaa Arg Ala Xaa Xaa Pro Ala
    130                 135                 140

Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Gly Ser Xaa Leu Lys Xaa
145                 150                 155                 160

Lys Pro Pro Lys Lys Pro Xaa Xaa Xaa Xaa Glu Xaa Gln Xaa Leu Pro
            165                 170                 175

Leu Gly Asn Gly Ile Gln Thr Met Xaa Ala Ser Val Gln Arg Ala Val
            180                 185                 190

Xaa Xaa Xaa Ser Gly Asp Val Pro Gly Xaa Arg Gly Ala Val Glu Gly
            195                 200                 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Xaa Ser Lys Lys Cys Ile
    210                 215                 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Xaa Lys Phe Glu Asp Xaa Ser
225                 230                 235                 240

Gly Xaa Xaa Lys Asn Lys Ala Arg Ser Xaa Ser Xaa Xaa Lys Pro Xaa
            245                 250                 255

Val Arg Ala Lys Gly Ala Gln Xaa Xaa Xaa Pro Gly Xaa Xaa Glu Xaa
            260                 265                 270
```

```
Xaa Xaa Gly Gln Gln Xaa Xaa Val Pro Xaa Xaa Xaa Xaa Leu Pro Ser
        275             280             285

Xaa Pro Gln Xaa Xaa Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Xaa
    290             295             300

Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His
305             310             315                 320

Leu Ala Cys Leu Ser Pro Pro Leu Xaa Glu Ile Pro Ser Gly Xaa Trp
            325             330                 335

Arg Cys Ser Xaa Cys Leu Gln Xaa Xaa Val Gln Xaa Xaa Xaa Xaa Xaa
            340             345             350

Xaa Glu Xaa Xaa Arg Pro Xaa Glu Xaa Pro Xaa Glu Thr Pro Xaa Xaa
        355             360             365

Xaa Gly Leu Arg Ser Ala Xaa Glu Xaa Xaa Arg Gly Pro Xaa Xaa Glu
    370             375             380

Xaa Xaa Ala Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Xaa Xaa Leu Xaa Ala
385             390             395                 400

Pro Xaa Xaa Ala Ala Pro Leu Xaa Xaa Leu Xaa Xaa Ser Ala Leu Xaa
        405             410             415

Pro Leu Leu Xaa Xaa Gly Xaa Glu Gly Xaa Xaa Xaa Xaa Ala Pro Xaa
        420             425             430

Ala Arg Cys Xaa Val Cys Gly Asp Gly Thr Xaa Val Leu Arg Cys Xaa
        435             440             445

His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Xaa Xaa Xaa
    450             455             460

Xaa Arg Pro Gly Thr Xaa Leu Arg Cys Xaa Ser Cys Ser Xaa Asp Xaa
465             470             475                 480

Thr Pro Xaa Pro Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Ser Xaa Xaa
            485             490             495

Arg Xaa Ala Pro Gly Xaa Ala Lys Xaa Xaa Asp Asp Xaa Ala Ser His
        500             505             510

Xaa Pro Xaa Leu His Arg Asp Asp Leu Glu Ser Leu Leu Xaa Glu His
    515             520             525

Xaa Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Xaa Arg Pro
    530             535             540

Xaa Ala Xaa Xaa Pro Xaa
545             550

<210>   11
<211>   48
<212>   DNA
<213>   Mouse

<400>   11
```

ggggcctcga tgga cgtctc tggggcccag gtcgtggttc gcgcgcta   48

<210> 12
<211> 15
<212> PRT
<213> Mouse

<400> 12

Pro Glu Leu Pro Ala Glu Thr Pro Gly Pro Ala Pro Ser Ala Arg
1   5   10   15

<210> 13
<211> 43
<212> DNA
<213> Mouse

<400> 13
agtgagcccc aggt taacca gaacg aggat gagtgt gccg tgt   43

<210> 14
<211> 14
<212> PRT
<213> Mouse

<400> 14

Ser Glu Pro Gln Val Asn Gln Asn Glu Asp Glu Cys Ala Val
1   5   10

<210> 15
<211> 48
<212> DNA
<213> Mouse

<400> 15
gtcaccaggc tcgg ttccct cgggt cccat ctctac tcgt ctttcacc   48

<210> 16
<211> 15
<212> PRT
<213> Mouse

<400> 16

Val Val Arg Ala Lys Gly Ala Gln Gly Arg Asp Glu Gln Lys Val
1   5   10   15

<210> 17
<211> 20
<212> DNA
<213> Artificial sequence

<400> 17
agaagtgcat ccag gttggc   20

<210> 18

```
<211>  20
<212>  DNA
<213>  Artificial sequence

<400>  18
ggaagagggg cgtcagcaat                                              20


<210>  19
<211>  15
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic peptide

<400>  19

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg
1                5                  10                  15


<210>  20
<211>  14
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic peptide

<400>  20

Ser Gln Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys
1                5                  10


<210>  21
<211>  19
<212>  DNA
<213>  Artificial sequence

<220>
<223>  B127FR4-29 primer for PCR

<400>  21
gctctggatg gcctactgc                                               19


<210>  22
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<223>  B127FR4-17 primer for PCR

<400>  22
agaagtgcat ccaggttggc                                              20


<210>  23
<211>  19
<212>  DNA
```

<213> Artificial sequence

<220>
<223> B127FR4-33 primer for PCR

<400> 23
gtgtgctcgc tcag aaggg   19

<210> 24
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer Mforw4 for PCR

<400> 24
tggcaggtgg ggat ggaa   18

<210> 25
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer Mrev15 for PCR

<400> 25
ggagggatgg aagg ggagga   20

<210> 26
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Forward primer Mforw2 for PCR

<400> 26
tcccacctga agac taagc   19

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse primer Mrev32 for PCR

<400> 27
tcacagctct ctgg acagaa   20

<210> 28
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Primer B127FR4-21 for PCR

<400> 28   18
ggcttctgag gctgcacc

<210> 29
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Double-paired finger motif

<400> 29

Cys Cys Cys Cys His Cys Cys Cys
1   5

<210> 30
<211> 42
<212> PRT
<213> Artificial sequence

<220>
<223> Structural motiff

<220>
<221> VARIANT
<222> (1)..(42)
<223> Xaa is any amino acid

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1   5   10   15

Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
        35   40